PCT 09

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/762,577A

DATE: 12/26/2002
TIME: 13:32:08

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF4\12262002\I762577A.raw

```
  4 <110> APPLICANT: Dranoff, Glenn
  5         Schmollinger, Jan
  6         Hodi, F. Stephen
  7         Mollick, Joseph
  9 <120> TITLE OF INVENTION: TUMOR ANTIGENS AND USES THEREOF
 12 <130> FILE REFERENCE: 2486/109 (formerly 50059/005002)
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/762,577A
C--> 14 <141> CURRENT FILING DATE: 2002-08-29
 14 <150> PRIOR APPLICATION NUMBER: 60/095,766
 15 <151> PRIOR FILING DATE: 1998-08-07
 17 <160> NUMBER OF SEQ ID NOS: 68
 19 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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ERRORED SEQUENCES

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495 <210> SEQ ID NO: 10
496 <211> LENGTH: 1168
497 <212> TYPE: PRT
498 <213> ORGANISM: Homo sapiens
500 <400> SEQUENCE: 10
501 Asn Ile Asp Leu Asp Leu Glu Ile Val Gln Ser Leu Gln His Gly His
502  1               5                  10                  15
503 Gly Gly Trp Thr Asp Gly Met Phe Glu Thr Leu Thr Thr Thr Gly Thr
504             20                  25                  30
505 Val Cys Gly Ile Asp Glu Asp His Asp Ile Val Val Gln Tyr Pro Ser
506         35                  40                  45
507 Gly Asn Arg Trp Thr Phe Asn Pro Ala Val Leu Thr Lys Ala Asn Ile
508     50                  55                  60
509 Val Arg Ser Gly Asp Ala Ala Gln Gly Ala Glu Gly Gly Thr Ser Gln
510 65                  70                  75                  80
511 Phe Gln Val Gly Asp Leu Val Gln Val Cys Tyr Asp Leu Glu Arg Ile
512                 85                  90                  95
513 Lys Leu Leu Gln Arg Gly His Gly Glu Trp Ala Glu Ala Met Leu Pro
514             100                 105                 110
515 Thr Leu Gly Lys Val Gly Arg Val Gln Gln Ile Tyr Ser Asp Ser Asp
516         115                 120                 125
517 Leu Lys Val Glu Val Cys Gly Thr Ser Trp Thr Tyr Asn Pro Ala Ala
518     130                 135                 140
519 Val Ser Lys Val Ala Ser Ala Gly Ser Ala Ile Ser Asn Ala Ser Gly
520 145                 150                 155                 160
521 Glu Arg Leu Ser Gln Leu Leu Lys Lys Leu Phe Glu Thr Gln Glu Ser
522                 165                 170                 175
```

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```
621  Leu Phe Ser Arg Phe Lys Arg Asn Ile Val Glx Leu Glu Ser Asp Tyr
                         965             970             975
622                                          Lys Gly Lys Ile Ser Asn Asn
623  Gln Phe Gln Gly Asp Glx Glx Thr Arg             990
                     980             985
624                                          Arg Val Ser Ile Asn Trp Pro
625  Ser Gly Gln Leu Lys Arg Lys Lys Lys            1005
                 995            1000
626                                          Ile Tyr Thr Leu Phe Cys Ser Ala
627  Leu Thr Val Ala Phe Leu Thr Leu            1020
         1010            1015
628                                          Val Tyr Phe Arg Phe Ser Val
629  Ser Val Phe Lys Lys Asn Leu Glx Lys            1035
                      1030            1035
E--> 630 1025                                 Glx His Cys Pro Ile
631  Ile Thr Tyr Leu Gly Leu Ile Glx Pro Val Lys            1055
                         1045            1050
632                                          Val His Ser Ile Pro
633  Trp Thr Ser Glu Val Leu Phe Ser Phe Ala Asp            1070
                 1060            1065
634                                          Lys Ser Phe Leu Leu
635  Val Ile Cys Lys Ile Asn Ala Phe Ser Lys Lys Lys            1085
             1075            1080
636                                          Phe Cys Leu His Tyr Arg
637  Cys Ile Ser Glx Phe Glx Gln Cys Glx Glx            1100
         1090            1095
638                                          Ile Phe Cys Tyr Lys Glu
639  Pro Tyr Phe His Tyr Leu Phe Leu Tyr Ser            1120
                      1110            1115
E--> 640 1105
641  Asn Ser Leu Ser Val Tyr Thr Tyr Gly Glx Gly Tyr Tyr Leu Asn Cys
                      1125            1130            1135
642                                          Asn Tyr Lys Tyr Phe Arg
643  Gln Gln Tyr Pro Arg His Gly Gln Glx Pro            1150
                 1140            1145
644                                          Asn Val Cys Leu Pro Val Asp Phe
645  Lys Ser Asp Gln Asp Met Tyr Arg            1165
             1155            1160
646
1510 <210> SEQ ID NO: 40
1511 <211> LENGTH: 309
1512 <212> TYPE: DNA
1513 <213> ORGANISM: Homo sapiens
1515 <400> SEQUENCE: 40
E--> 1516  ncaaagtcaa atgaatttat tcagaaaagg ccttgcttgg tatcagacta agaaaagcag   60
E--> 1517  ccctgcccgc cgccccccan tccagaaggg tcaatttaca aagacagggg cgcaggggag  120
1518       agctgggtgg ggaagacaca gccaggccag gagcttctgc aggccttggg cttccctgag  180
1519       ggcctcgcgg cttctgggtg gctgctatag tggccccaca ggaggccatg cactgtgggg  240
E--> 1520  gtcattgggt cacngggtca cgaangcata gcctnagggg gnagcccgtn agcagctccg  300
E--> 1521  gganggccc                                                           309
1533 <210> SEQ ID NO: 42
1534 <211> LENGTH: 166
1535 <212> TYPE: DNA
1536 <213> ORGANISM: Homo sapiens
1538 <400> SEQUENCE: 42
E--> 1539  cggcctgcag aagcntcctg gncntggttg ttttttcccc acccagctct cccctgcgcc   60
E--> 1540  cctttttttt taaatnnacc cttctggagt ggggggcggc gggcagggct gctttttttna  120
E--> 1541  gtctgatgcc aagcaaggcc ttttttgaat aanttcattt ganttt              166
1543 <210> SEQ ID NO: 43
1544 <211> LENGTH: 209
1545 <212> TYPE: DNA
1546 <213> ORGANISM: Homo sapiens
```

move over to the left, one space, and add the "Ø".
←1040
←1120

N's detected, see p. 11 for explanation

some error

```
   1548  <400> SEQUENCE: 43                                                              60
E--> 1549  gaaggtggat nagggtgctg tggacagtgc tacggtggcc agtggtggtg cccagacctt            120
E--> 1550  ggcccttgcc gggtcccctg ccccatcgcn cggccaaggc tggacacagt gagaacgggg            180
E--> 1551  ttgaggagga cacagaangt caaacggggc ccaaagaagg tacccntggg gagcccatca            209
E--> 1552  gagancccan gccccagccn ggcagggac
   1674  <210> SEQ ID NO: 46
   1675  <211> LENGTH: 1299
   1676  <212> TYPE: PRT
   1677  <213> ORGANISM: Homo sapiens
   1679  <400> SEQUENCE: 46
   1680  Met Glu Pro Pro Ser Cys Ile Gln Asp Glu Pro Phe Pro His Pro Leu
   1681   1               5                  10                  15
   1682  Glu Pro Glu Pro Gly Val Ser Ala Gln Pro Gly Pro Gly Lys Pro Ser
   1683          20                  25                  30
   1684  Asp Lys Arg Phe Arg Leu Trp Tyr Val Gly Gly Ser Cys Leu Asp His
   1685          35                  40                  45
   1686  Arg Thr Thr Leu Pro Met Leu Pro Trp Leu Met Ala Glu Ile Arg Arg
   1687          50                  55                  60
   1688  Arg Ser Gln Lys Pro Glu Ala Gly Gly Cys Gly Ala Pro Ala Ala Arg
   1689   65                  70                  75                  80
   1690  Glu Val Ile Leu Val Leu Ser Ala Pro Phe Leu Arg Cys Val Pro Ala
   1691                  85                  90                  95
   1692  Pro Gly Ala Gly Ala Ser Gly Gly Thr Ser Pro Ser Ala Thr Gln Pro
   1693          100                 105                 110
   1694  Asn Pro Ala Val Phe Ile Phe Glu His Lys Ala Gln His Ile Ser Arg
   1695          115                 120                 125
   1696  Phe Ile His Asn Ser His Asp Leu Thr Tyr Phe Ala Tyr Leu Ile Lys
   1697          130                 135                 140
   1698  Ala Gln Pro Asp Asp Pro Glu Ser Gln Met Ala Cys His Val Phe Arg
   1699  145                 150                 155                 160
   1700  Ala Thr Asp Pro Ser Gln Val Pro Asp Val Ile Ser Ser Ile Arg Gln
   1701                  165                 170                 175
   1702  Leu Ser Lys Ala Ala Met Lys Glu Asp Ala Lys Pro Ser Lys Asp Asn
   1703          180                 185                 190
   1704  Glu Asp Ala Phe Tyr Asn Ser Gln Lys Phe Glu Val Leu Tyr Cys Gly
   1705          195                 200                 205
   1706  Lys Val Thr Val Thr His Lys Lys Ala Pro Ser Ser Leu Ile Asp Asp
   1707          210                 215                 220
   1708  Cys Met Glu Lys Phe Ser Leu His Glu Gln Gln Arg Leu Lys Ile Gln
   1709  225                 230                 235                 240
   1710  Gly Glu Gln Arg Gly Pro Asp Pro Gly Glu Asp Leu Ala Asp Leu Glu
   1711                  245                 250                 255
   1712  Val Val Val Pro Gly Ser Pro Gly Asp Cys Leu Pro Glu Glu Ala Asp
   1713                  260                 265                 270
   1714  Gly Thr Asp Thr His Leu Gly Leu Pro Ala Gly Ala Ser Gln Pro Ala
   1715          275                 280                 285
   1716  Leu Thr Ser Ser Arg Val Cys Phe Pro Glu Arg Ile Leu Glu Asp Ser
   1717          290                 295                 300
   1718  Gly Phe Asp Glu Gln Gln Glu Phe Arg Ser Arg Cys Ser Ser Val Thr
```

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1768 Ala Pro Ser Phe Thr Ala Pro Ser Phe Leu Lys Ser Phe Tyr Gln Asn
1769 705             710             715                 720
1770 Ser Gly Arg Leu Ser Pro Gln Tyr Glu Asn Glu Ile Arg Gln Asp Thr
1771             725             730                 735
1772 Ala Ser Glu Ser Ser Asp Gly Glu Gly Arg Lys Arg Thr Ser Ser Thr
1773             740             745                 750
1774 Cys Ser Asn Glu Ser Leu Ser Val Gly Gly Thr Ser Val Thr Pro Arg
1775             755             760                 765
1776 Arg Ile Ser Trp Arg Gln Arg Ile Phe Leu Arg Val Ala Ser Pro Met
1777         770             775             780
1778 Asn Lys Ser Pro Ser Ala Met Gln Gln Gln Asp Gly Leu Asp Arg Asn
1779 785             790             795                 800
1780 Glu Leu Leu Pro Leu Ser Pro Leu Ser Pro Thr Met Glu Glu Glu Pro
1781             805             810             815
1782 Leu Val Ile Phe Leu Ser Gly Glu Asp Asp Pro Glu Lys Ile Glu Glu
1783             820             825             830
1784 Arg Lys Lys Ser Lys Glu Leu Arg Ser Leu Trp Arg Lys Ala Ile His
1785             835             840             845
1786 Gln Gln Ile Leu Leu Leu Arg Met Glu Lys Glu Asn Gln Lys Leu Glu
1787         850             855             860
1788 Gly Ala Ser Arg Asp Glu Leu Gln Ser Arg Lys Val Lys Leu Asp Tyr
1789 865             870             875                 880
1790 Glu Glu Val Gly Ala Cys Gln Lys Glu Val Leu Ile Thr Trp Asp Lys
1791             885             890                 895
1792 Lys Leu Leu Asn Cys Arg Ala Lys Ile Arg Cys Asp Met Glu Asp Ile
1793             900             905             910
1794 His Thr Leu Leu Lys Glu Gly Val Pro Lys Ser Arg Arg Gly Glu Ile
1795             915             920             925
1796 Trp Gln Phe Leu Ala Leu Gln Tyr Arg Leu Arg His Arg Leu Pro Asn
1797         930             935             940
1798 Lys Gln Gln Pro Pro Asp Ile Ser Tyr Lys Glu Leu Leu Lys Gln Leu
1799 945             950             955                 960
1800 Thr Ala Gln Gln His Ala Ile Leu Val Asp Leu Gly Arg Thr Phe Pro
1801             965             970             975
1802 Thr His Pro Tyr Phe Ser Val Gln Leu Gly Pro Gly Gln Leu Ser Leu
1803             980             985             990
1804 Phe Asn Leu Leu Lys Ala Tyr Ser Leu Leu Asp Lys Glu Val Gly Tyr
1805             995             1000            1005
1806 Cys Gln Gly Ile Ser Phe Val Ala Gly Val Leu Leu Leu His Met Ser
1807         1010            1015            1020
1808 Glu Glu Gln Ala Phe Glu Met Leu Lys Phe Leu Met Tyr Asp Leu Gly
```
E--> 1809 1025   1030   1035   ←1040
```
1810 Phe Arg Lys Gln Tyr Arg Pro Asp Met Met Ser Leu Gln Ile Gln Met
1811             1045            1050            1055
1812 Tyr Gln Leu Ser Arg Leu Leu His Asp Tyr His Arg Asp Leu Tyr Asn
1813             1060            1065            1070
1814 His Leu Glu Glu Asn Glu Ile Ser Pro Ser Leu Tyr Ala Ala Pro Trp
1815             1075            1080            1085
1816 Phe Leu Thr Leu Phe Ala Ser Gln Phe Ser Leu Gly Phe Val Ala Arg
```

```
      1817    1090                1095              1100
      1818  Val Phe Asp Ile Ile Phe Leu Gln Gly Thr Glu Val Ile Phe Lys Val
E--> 1819  1105              1110              1115              ←1120
      1820  Ala Leu Ser Leu Leu Ser Ser Gln Glu Thr Leu Ile Met Glu Cys Glu
      1821                1125              1130              1135
      1822  Ser Phe Glu Asn Ile Val Glu Phe Leu Lys Asn Thr Leu Pro Asp Met
      1823            1140              1145              1150
      1824  Asn Thr Ser Glu Met Glu Lys Ile Ile Thr Gln Val Phe Glu Met Asp
      1825        ·1155              1160              1165
      1826  Ile Ser Lys Gln Leu His Ala Tyr Glu Val Glu Tyr His Val Leu Gln
      1827      1170              1175              1180
      1828  Asp Glu Leu Gln Glu Ser Ser Tyr Ser Cys Glu Asp Ser Glu Thr Leu
E--> 1829  1185              1190              1195              ←1200
      1830  Glu Lys Leu Glu Arg Ala Asn Ser Gln Leu Lys Arg Gln Asn Met Asp
      1831                1205              1210              1215
      1832  Leu Leu Glu Lys Leu Gln Val Ala His Thr Lys Ile Gln Ala Leu Glu
      1833            1220              1225              1230
      1834  Ser Asn Leu Glu Asn Leu Leu Thr Arg Glu Thr Lys Met Lys Ser Leu
      1835          1235              1240              1245
      1836  Ile Arg Thr Leu Glu Gln Glu Lys Met Ala Tyr Gln Lys Thr Val Glu
      1837        1250              1255              1260
      1838  Gln Leu Arg Lys Leu Leu Pro Ala Asp Ala Leu Ala Asn Cys Asp Leu
E--> 1839  1265              1270              1275              ←1280
      1840  Leu Leu Arg Asp Leu Asn Cys Asn Pro Asn Asn Lys Ala Lys Ile Gly
      1841                1285              1290              1295
      1842  Asn Lys Pro
      1969  <210> SEQ ID NO: 49
      1970  <211> LENGTH: 226
      1971  <212> TYPE: DNA
      1972  <213> ORGANISM: Homo sapiens
      1974  <400> SEQUENCE: 49
      1975  ctgggatact cccctcccag ggtgtctggt ggcaggcctg tgcctatccc tgctgtcccc    60
      1976  agggtgggcc ccgggggtca ggagctccag aagggccagc tgggcatatt ctgagattgg   120
E--> 1977  ccatcagccc ccatttctgc tgcaaacctg gtcagagcca gtnttccntc catgggacct   180
      1978  aaagacagtg ccaagtgcct gcaccgtgga ccacagccga gccact              226
      2262  <210> SEQ ID NO: 62
      2263  <211> LENGTH: 607
      2264  <212> TYPE: DNA
      2265  <213> ORGANISM: Homo sapiens
      2267  <400> SEQUENCE: 62
      2268  ttttcagcat gagaatatgt gaatatgttt atttaggttt aacttacttc ttactatata    60
      2269  gatttggctt gttttttata ataacaactg atatatgatt cacaaaaaag cagagaagag   120
      2270  taagagaaag agagagaaat ggagaaagag aagaaaaaag ggataaagaa tgaaagagag   180
      2271  aaagagaata ccattctcta aaggaagagg tgcagaaaat tccattatcc tttcttcttg   240
      2272  atcatgcctt gtatgattgg cagccaaact agcccactgt gaaacccaac gtttgcttcc   300
      2273  agatgaagat gtgccttcct ctgagtggtg aaatccagat gtagtcagtg gttttctttc   360
      2274  ttccattact gctgcagcag aactgagagc ccaatctttt attagatctt tatgtttttc   420
      2275  gttgataaca ggcctattat aatccgattg tcatctactc caaacacaac agctggtctg   480·
      2276  atgctttcag tagccggacc tctgtagctt ttgtgttcga atggtggcgt ctaagtgttc   540
```

— No found →See p II

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```
2277  ctcaagagtt gcacgtttgc tacagcgccg tgagccccag cgttctctga atcacttgcg    600
                                                                           607
E--> 2278  tncatca
     2280  <210> SEQ ID NO: 63
     2281  <211> LENGTH: 402
     2282  <212> TYPE: DNA
     2283  <213> ORGANISM: Homo sapiens
     2285  <400> SEQUENCE: 63
E--> 2286  ggcagagcac agaccaagcc aggagatgga taaaggttaa aaaatcaagc aacttctgct    60
     2287  acttctgaaa aggataatga tgatgaccaa agtgacaagg gtacttatac cattgagtta   120
     2288  gagaatccca acagtgagga agtggaagca agaaaaatga ttcacaaggt aaataattga   180
     2289  aatttgagtg tgatcttagt tgttgtgtgg tgtatttgac tggtggaaat tattggagag   240
     2290  tcagcatgag atgttgtcat gcagtcagtg gtatgtgaat tttaggtttt tattagggaa   300
     2291  ctgcaagact aacagtaaga ccaacatgct ttgtgatttt atttgctgat attctgaatt   360
     2292  tacctgagtt tcatacataa agctctgtac atttaaaagg tt                      402
     2294  <210> SEQ ID NO: 64
     2295  <211> LENGTH: 607
     2296  <212> TYPE: DNA
     2297  <213> ORGANISM: Homo sapiens
     2299  <400> SEQUENCE: 64
     2300  ttttcagcat gagaatatgt gaatatgttt atttaggttt aacttacttc ttactatata   60
     2301  gatttggctt gttttttata ataacaactg atatatgatt cacaaaaaag cagagaagag   120
     2302  taagagaaag agagagaaat ggagaaagag aagaaaaaag ggataaagaa tgaaagagag   180
     2303  aaagagaata ccattctcta aaggaagagg tgcagaaaat tccattatcc tttcttcttg   240
     2304  atcatgcctt gtatgattgg cagccaaact agcccactgt gaaacccaac gtttgcttcc   300
     2305  agatgaagat gtgccttcct ctgagtggtg aaatccagat gtagtcagtg gtttctttc    360
     2306  ttccattact gctgcagcag aactgagagc ccaatctttt attagatctt tatgtttttc   420
     2307  gttgataaca ggcctattat aatccgattg tcatctactc caaacacaac agctggtctg   480
     2308  atgctttcag tagccggacc tctgtagctt ttgtgttcga atggtggcgt ctaagtgttc   540
     2309  ctcaagagtt gcacgtttgc tacagcgccg tgagccccag cgttctctga atcacttgcg   600
                                                                           607
E--> 2310  tncatca
     2312  <210> SEQ ID NO: 65
     2313  <211> LENGTH: 317
     2314  <212> TYPE: DNA
     2315  <213> ORGANISM: Homo sapiens
     2317  <400> SEQUENCE: 65
E--> 2318  tggggcgtgt gtggaanaac gttantgccc agcggantag nggcccccgga gcncgaccgc   60
E--> 2319  agcggcanan cgacaacagc ggcgacgacg acgacgacga ggtgggggga ggacggcgtg   120
E--> 2320  cgagagactc acgggacgcg acgnccccgc ctcccccgtc cggtccctct ctccacggta   180
     2321  aggggatgac gtagctttgc caaagactta gaagctaagc agaaaatgag cttaacatcc   240
     2322  tggttttttgg tgagcagtgg aggcactcgc cacaggctgc cacgagaaat gattttttgtt   300
     2323  ggaaaaaatg actgtga                                                  317
     2473  <210> SEQ ID NO: 68
     2474  <211> LENGTH: 2349
     2475  <212> TYPE: PRT
     2476  <213> ORGANISM: Homo sapiens
     2478  <400> SEQUENCE: 68
     2479  Met Ala Ala Val Leu Gln Gln Val Leu Glu Arg Thr Glu Leu Asn Lys
     2480    1           5                  10                  15
     2481  Leu Pro Lys Ser Val Gln Asn Lys Leu Glu Lys Phe Leu Ala Asp Gln
```

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```
                         805                    810                    815
2580                                                    Glu Arg Ser Glu Thr Glu
2581     Thr Asn Leu Gln Thr Ile Gln Gly Ile Leu              830
            820                        825    Ile Glu Lys Leu Glu His Glu Ile
2582
2583     Thr Lys Gln Arg Leu Ser Ser Gln         845
            835                        840    Glu Asn Glu Val Glu Gln Arg His Thr
2584
2585     Ser His Leu Lys Lys Lys Leu          860
            850                    855    Gln Leu Leu Asp Thr Lys Arg Gln Leu
2586
2587     Leu Thr Arg Asn Leu Asp Val              875              880
            865                870    Lys Glu Leu Leu Lys Asn
2588
2589     Asp Thr Glu Thr Asn Leu His Leu Asn Thr          895
            885                        890    Gln His Leu Ser Asn Met Glu
2590
2591     Ala Gln Lys Glu Ile Ala Thr Leu Lys          910
            900                    905    Gly Lys Gly Gln Pro
2592
2593     Val Gln Val Ala Ser Gln Ser Ser Gln Arg Thr          925
            915                    920    Ser Gln Leu Arg Gln Thr
2594
2595     Ser Asn Lys Glu Asp Val Asp Asp Leu Val Ser          940
            930                    935    Lys Thr Ser Thr Ser
2596
2597     Glu Glu Gln Val Asn Asp Leu Lys Glu Arg Leu          960
            945                950    Leu Glu Glu Ser Leu
2598
2599     Asn Val Glu Gln Tyr Gln Ala Met Val Thr Ser          975
                        965                    970    Val Arg Lys Asn Ile Glu Val
2600
2601     Asn Lys Glu Lys Gln Val Thr Glu Glu          990
                    980                    985    Leu Glu Lys Lys Leu
2602
2603     Arg Leu Lys Glu Ser Ala Glu Phe Gln Thr Gln         1005
            995                    1000    Gln Glu Leu Gln Asp Asp Lys Arg Arg
2604
2605     Met Glu Val Glu Lys Glu Lys Gln Glu Leu         1020
            1010                    1015    Glu Leu Lys Lys Thr Leu
2606
2607     Ala Ile Glu Ser Met Glu Gln Gln Leu Ser         ←1040
E-->2608     1025                    1030                1035
2609     Ser Ser Val Gln Asn Glu Val Gln Glu Ala Leu Gln Arg Ala Ser Thr
                        1045                    1050                1055
2610
2611     Ala Leu Ser Asn Glu Gln Gln Ala Arg Arg Asp Cys Gln Glu Gln Ala
            1060                    1065                1070
2612
2613     Lys Ile Ala Val Glu Ala Gln Asn Lys Tyr Glu Arg Glu Leu Met Leu
            1075                    1080                1085
2614
2615     His Ala Ala Asp Val Glu Ala Leu Gln Ala Ala Lys Glu Gln Val Ser
            1090                    1095                1100
2616
2617     Lys Met Ala Ser Val Arg Gln His Leu Glu Glu Thr Thr Gln Lys Ala
                        1110                    1115                ←1120
E-->2618     1105
2619     Glu Ser Gln Leu Leu Glu Cys Lys Ala Ser Trp Glu Glu Arg Glu Arg
                        1125                    1130                1135
2620
2621     Met Leu Lys Asp Glu Val Ser Lys Cys Val Cys Arg Cys Glu Asp Leu
            1140                    1145                1150
2622
2623     Glu Lys Gln Asn Arg Leu Leu His Asp Gln Ile Glu Lys Leu Ser Asp
            1155                    1160                1165
2624
2625     Lys Val Val Ala Ser Val Lys Glu Gly Val Gln Gly Pro Leu Asn Val
            1170                    1175                1180
2626
2627     Ser Leu Ser Glu Glu Gly Lys Ser Gln Glu Gln Ile Leu Glu Ile Leu
                        1190                    1195                ←1200
E-->2628     1185
```

```
       2629   Arg Phe Ile Arg Arg Glu Lys Glu Ile Ala Glu Thr Arg Phe Glu Val
       2630                              1205                1210                1215
       2631   Ala Gln Val Glu Ser Leu Arg Tyr Arg Gln Arg Val Glu Leu Leu Glu
       2632                  1220                1225                1230
       2633   Arg Glu Leu Gln Glu Leu Glu Asp Ser Leu Asn Ala Glu Arg Glu Lys
       2634                  1235                1240                1245
       2635   Val Gln Val Thr Ala Lys Thr Met Ala Gln His Glu Glu Leu Met Lys
       2636         1250                1255                1260
       2637   Lys Thr Glu Thr Met Asn Val Val Met Glu Thr Asn Lys Met Leu Arg
E-->   2638   1265                1270                1275                  1280
       2639   Glu Glu Lys Glu Arg Leu Glu Gln Asp Leu Gln Gln Met Gln Ala Lys
       2640                  1285                1290                1295
       2641   Val Arg Lys Leu Glu Leu Asp Ile Leu Pro Leu Gln Glu Ala Asn Ala
       2642                  1300                1305                1310
       2643   Glu Leu Ser Glu Lys Ser Gly Met Leu Gln Ala Glu Lys Lys Leu Leu
       2644                  1315                1320                1325
       2645   Glu Glu Asp Val Lys Arg Trp Lys Ala Arg Asn Gln His Leu Val Ser
       2646         1330                1335                1340
       2647   Gln Gln Lys Asp Pro Asp Thr Glu Glu Tyr Arg Lys Leu Leu Ser Glu
E-->   2648   1345                1350                1355                  1360
       2649   Lys Glu Val His Thr Lys Arg Ile Gln Gln Leu Thr Glu Glu Ile Gly
       2650                  1365                1370                1375
       2651   Arg Leu Lys Ala Glu Ile Ala Arg Ser Asn Ala Ser Leu Thr Asn Asn
       2652                  1380                1385                1390
       2653   Gln Asn Leu Ile Gln Ser Leu Lys Glu Asp Leu Asn Lys Val Arg Thr
       2654                  1395                1400                1405
       2655   Glu Lys Glu Thr Ile Gln Lys Asp Leu Asp Ala Lys Ile Ile Asp Ile
       2656         1410                1415                1420
       2657   Gln Glu Lys Val Lys Thr Ile Thr Gln Val Lys Lys Ile Gly Arg Arg
E-->   2658   1425                1430                1435                  1440
       2659   Tyr Lys Thr Gln Tyr Glu Glu Leu Lys Ala Gln Gln Asp Lys Val Met
       2660                  1445                1450                1455
       2661   Glu Thr Ser Ala Gln Ser Ser Gly Asp His Gln Glu Gln His Val Ser
       2662                  1460                1465                1470
       2663   Val Gln Glu Met Gln Glu Leu Lys Glu Thr Leu Asn Gln Ala Glu Thr
       2664         1475                1480                1485
       2665   Lys Ser Lys Ser Leu Glu Ser Gln Val Glu Asn Leu Gln Lys Thr Leu
       2666         1490                1495                1500
       2667   Ser Glu Lys Glu Thr Glu Ala Arg Asn Leu Gln Glu Gln Thr Val Gln
E-->   2668   1505                1510                1515                  1520
       2669   Leu Gln Ser Glu Leu Ser Arg Leu Arg Gln Asp Leu Gln Asp Arg Thr
       2670                  1525                1530                1535
       2671   Thr Gln Glu Glu Gln Leu Arg Gln Gln Ile Thr Glu Lys Glu Glu Lys
       2672                  1540                1545                1550
       2673   Thr Arg Lys Ala Ile Val Ala Ala Lys Ser Lys Ile Ala His Leu Ala
       2674         1555                1560                1565
       2675   Gly Val Lys Asp Gln Leu Thr Lys Glu Asn Glu Glu Leu Lys Gln Arg
       2676         1570                1575                1580
       2677   Asn Gly Ala Leu Asp Gln Gln Lys Asp Glu Leu Asp Val Arg Ile Thr
```

12/26/02

RAW SEQUENCE LISTING   DATE: 12/26/2002
PATENT APPLICATION: US/09/762,577A   TIME: 13:32:08

```
              Input Set : A:\pto.vsk.txt
              Output Set: N:\CRF4\12262002\I762577A.raw


E--> 2678  1585              1590              1595              1600
     2679  Ala Leu Lys Ser Gln Tyr Glu Gly Arg Ile Ser Arg Leu Glu Arg Glu
     2680              1605              1610              1615
     2681  Leu Arg Glu His Gln Glu Arg His Leu Glu Gln Arg Asp Glu Pro Gln
     2682              1620              1625              1630
     2683  Glu Pro Ser Asn Lys Val Pro Glu Gln Gln Arg Gln Ile Thr Leu Lys
     2684              1635              1640              1645
     2685  Thr Thr Pro Ala Ser Gly Glu Arg Gly Ile Ala Ser Thr Ser Asp Pro
     2686              1650              1655              1660
     2687  Pro Thr Ala Asn Ile Lys Pro Thr Pro Val Val Ser Thr Pro Ser Lys
E--> 2688  1665              1670              1675              1680
     2689  Val Thr Ala Ala Ala Met Ala Gly Asn Lys Ser Thr Pro Arg Ala Ser
     2690              1685              1690              1695
     2691  Ile Arg Pro Met Val Thr Pro Ala Thr Val Thr Asn Pro Thr Thr Thr
     2692              1700              1705              1710
     2693  Pro Thr Ala Thr Val Met Pro Thr Thr Gln Val Glu Ser Gln Glu Ala
     2694              1715              1720              1725
     2695  Met Gln Ser Glu Gly Pro Val Glu His Val Pro Val Phe Gly Ser Thr
     2696              1730              1735              1740
     2697  Ser Gly Ser Val Arg Ser Thr Ser Pro Asn Val Gln Pro Ser Ile Ser
E--> 2698  1745              1750              1755              1760
     2699  Gln Pro Ile Leu Thr Val Gln Gln Gln Thr Gln Ala Thr Ala Phe Val
     2700              1765              1770              1775
     2701  Gln Pro Thr Gln Gln Ser His Pro Gln Ile Glu Pro Ala Asn Gln Glu
     2702              1780              1785              1790
     2703  Leu Ser Ser Asn Ile Val Glu Val Val Gln Ser Ser Pro Val Glu Arg
     2704              1795              1800              1805
     2705  Pro Ser Thr Ser Thr Ala Val Phe Gly Thr Val Ser Ala Thr Pro Ser
     2706              1810              1815              1820
     2707  Ser Ser Leu Pro Lys Arg Thr Arg Glu Glu Glu Glu Asp Ser Thr Ile
E--> 2708  1825              1830              1835              1840
     2709  Glu Ala Ser Asp Gln Val Ser Asp Asp Thr Val Glu Met Pro Leu Pro
     2710              1845              1850              1855
     2711  Lys Lys Leu Lys Ser Val Thr Pro Val Gly Thr Glu Glu Glu Val Met
     2712              1860              1865              1870
     2713  Ala Glu Glu Ser Thr Asp Gly Glu Val Glu Thr Gln Val Tyr Asn Gln
     2714              1875              1880              1885
     2715  Asp Ser Gln Asp Ser Ile Gly Glu Gly Val Thr Gln Gly Asp Tyr Thr
     2716              1890              1895              1900
     2717  Pro Met Glu Asp Ser Glu Glu Thr Ser Gln Ser Leu Gln Ile Asp Leu
E--> 2718  1905              1910              1915              1920
     2719  Gly Pro Leu Gln Ser Asp Gln Gln Thr Thr Thr Ser Ser Gln Asp Gly
     2720              1925              1930              1935
     2721  Gln Gly Lys Gly Asp Asp Val Ile Val Ile Asp Ser Asp Asp Glu Glu
     2722              1940              1945              1950
     2723  Glu Asp Glu Glu Asp Asp Asp Asp Glu Asp Asp Thr Gly Met Gly
     2724              1955              1960              1965
     2725  Asp Glu Gly Glu Asp Ser Asn Glu Gly Thr Gly Ser Ala Asp Gly Asn
     2726              1970              1975              1980
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RAW SEQUENCE LISTING   DATE: 12/26/2002
PATENT APPLICATION: US/09/762,577A   TIME: 13:32:08

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF4\12262002\I762577A.raw

```
      2727  Asp Gly Tyr Glu Ala Asp Asp Ala Glu Gly Gly Asp Gly Thr Asp Pro
E--> 2728  1985            1990            1995            ◄2000
      2729  Gly Thr Glu Thr Glu Glu Ser Met Gly Gly Gly Glu Gly Asn His Arg
      2730            2005            2010            2015
      2731  Ala Ala Asp Ser Gln Asn Ser Gly Glu Gly Asn Thr Gly Ala Ala Glu
      2732            2020            2025            2030
      2733  Ser Ser Phe Ser Gln Glu Val Ser Arg Glu Gln Gln Pro Ser Ser Ala
      2734            2035            2040            2045
      2735  Ser Glu Arg Gln Ala Pro Arg Ala Pro Gln Ser Pro Arg Arg Pro Pro
      2736            2050            2055            2060
      2737  His Pro Leu Pro Pro Arg Leu Thr Ile His Ala Pro Pro Gln Glu Leu
E--> 2738  2065            2070            2075            ◄2080
      2739  Gly Pro Pro Val Gln Arg Ile Gln Met Thr Arg Arg Gln Ser Val Gly
      2740            2085            2090            2095
      2741  Arg Gly Leu Gln Leu Thr Pro Gly Ile Gly Gly Met Gln Gln His Phe
      2742            2100            2105            2110
      2743  Phe Asp Asp Glu Asp Arg Thr Val Pro Ser Thr Pro Thr Leu Val Val
      2744            2115            2120            2125
      2745  Pro His Arg Thr Asp Gly Phe Ala Glu Ala Ile His Ser Pro Gln Val
      2746            2130            2135            2140
      2747  Ala Gly Val Pro Arg Phe Arg Phe Gly Pro Pro Glu Asp Met Pro Gln
E--> 2748  2145            2150            2155            ◄2160
      2749  Thr Ser Ser Ser His Ser Asp Leu Gly Gln Leu Ala Ser Gln Gly Gly
      2750            2165            2170            2175
      2751  Leu Gly Met Tyr Glu Thr Pro Leu Phe Leu Ala His Glu Glu Glu Ser
      2752            2180            2185            2190
      2753  Gly Gly Arg Ser Val Pro Thr Thr Pro Leu Gln Val Ala Ala Pro Val
      2754            2195            2200            2205
      2755  Thr Val Phe Thr Glu Ser Thr Thr Ser Asp Ala Ser Glu His Ala Ser
      2756            2210            2215            2220
      2757  Gln Ser Val Pro Met Val Thr Thr Ser Thr Gly Thr Leu Ser Thr Thr
E--> 2758  2225            2230            2235            ◄2240
      2759  Asn Glu Thr Ala Thr Gly Asp Asp Gly Asp Glu Val Phe Val Glu Ala
      2760            2245            2250            2255
      2761  Glu Ser Glu Gly Ile Ser Ser Glu Ala Gly Leu Glu Ile Asp Ser Gln
      2762            2260            2265            2270
      2763  Gln Glu Glu Glu Pro Val Gln Ala Ser Asp Glu Ser Asp Leu Pro Ser
      2764            2275            2280            2285
      2765  Thr Ser Gln Asp Pro Pro Ser Ser Ser Ser Val Asp Thr Ser Ser Ser
      2766            2290            2295            2300
      2767  Gln Pro Lys Pro Phe Arg Arg Val Arg Leu Gln Thr Thr Leu Arg Gln
E--> 2768  2305            2310            2315            ◄2320
      2769  Gly Val Arg Gly Arg Gln Phe Asn Arg Gln Arg Gly Val Ser His Ala
      2770            2325            2330            2335
      2771  Met Gly Gly Arg Gly Gly Ile Asn Arg Gly Asn Ile Asn
      2772            2340            2345
      2777  02486/00109    215857.1
E--> 2780  1
```

—delete

VARIABLE LOCATION SUMMARY
PATENT APPLICATION: US/09/762,577A

DATE: 12/26/2002
TIME: 13:32:09

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF4\12262002\I762577A.raw

Use of n's or Xaa's(NEW RULES):
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:24; Xaa Pos. 2,4,7,16
Seq#:30; Xaa Pos. 9,14,15,20
Seq#:40; N Pos. 1,80,254,265,275,282,290,304
Seq#:42; N Pos. 15,22,24,76,77,119,153,163
Seq#:43; N Pos. 11,90,138,166,185,190,200
Seq#:49; N Pos. 163,168
Seq#:62; N Pos. 602
Seq#:63; N Pos. 35
Seq#:64; N Pos. 602
Seq#:65; N Pos. 17,25,37,41,53,68,70,144

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/762,577A**

DATE: 12/26/2002
TIME: 13:32:09

Input Set : **A:\pto.vsk.txt**
Output Set: **N:\CRF4\12262002\I762577A.raw**

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:630 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:1150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:1220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:1222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:16
L:1516 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:40
M:340 Repeated in SeqNo=40
L:1539 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:42
M:340 Repeated in SeqNo=42
L:1549 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:43
M:340 Repeated in SeqNo=43
L:1809 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46
M:332 Repeated in SeqNo=46
L:1977 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:49
L:2278 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:62
L:2286 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:63
L:2310 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:64
L:2318 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:65
M:340 Repeated in SeqNo=65
L:2608 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:68
M:332 Repeated in SeqNo=68
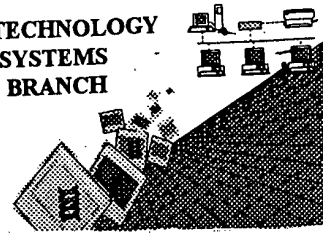
RAW SEQUENCE LISTING ERROR REPORT

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Revised 01/29/2002